

# Package: cgmquantify (via r-universe)

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**Type** Package

**Title** Analyzing Glucose and Glucose Variability

**Version** 0.1.0

**Imports** dplyr, tidyverse, ggplot2, hms, stats, magrittr

**Description** Continuous glucose monitoring (CGM) systems provide real-time, dynamic glucose information by tracking interstitial glucose values throughout the day. Glycemic variability, also known as glucose variability, is an established risk factor for hypoglycemia (Kovatchev) and has been shown to be a risk factor in diabetes complications. Over 20 metrics of glycemic variability have been identified. Here, we provide functions to calculate glucose summary metrics, glucose variability metrics (as defined in clinical publications), and visualizations to visualize trends in CGM data. Cho P, Bent B, Wittmann A, et al. (2020)

<[https://diabetes.diabetesjournals.org/content/69/Supplement\\_1/73-LB.abstract](https://diabetes.diabetesjournals.org/content/69/Supplement_1/73-LB.abstract)>  
American Diabetes Association (2020)  
<[https://professional.diabetes.org/diapro/glucose\\_calc](https://professional.diabetes.org/diapro/glucose_calc)>  
Kovatchev B (2019) <doi:10.1177/1932296819826111> Kovatchev BP (2017) <doi:10.1038/nrendo.2017.3> Tamborlane W V., Beck RW, Bode BW, et al. (2008) <doi:10.1056/NEJMoa0805017> Umpierrez GE, P. Kovatchev B (2018) <doi:10.1016/j.amjms.2018.09.010>.

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**Encoding** UTF-8

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**RoxigenNote** 7.1.1

**Suggests** testthat (>= 2.0.0), knitr, rmarkdown

**Config/testthat.edition** 2, devtools

**VignetteBuilder** knitr

**Depends** R (>= 2.10)

**NeedsCompilation** no

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**Repository** CRAN

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eA1c	<i>Compute Estimated A1c</i>
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### Description

This function computes the estimated A1c, according to the American Diabetes Association calculator

### Usage

```
eA1c(df)
```

### Arguments

df	Data frame read through readfile
----	----------------------------------

**Value**

A numeric value representing eA1c

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
eA1c(mydata)
```

---

GMI

*Compute Glycemic Management Indicator***Description**

This function computes the estimated GMI

**Usage**

```
GMI(df)
```

**Arguments**

df	Data frame read through readfile
----	----------------------------------

**Value**

A numeric value representing GMI

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
GMI(mydata)
```

---

HBGI

*Compute High Blood Glucose Index***Description**

This function computes the high blood glucose index

**Usage**

```
HBGI(df)
```

**Arguments**

**df** Data frame read through readfile

**Value**

A numeric value representing HBGI

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
HBGI(mydata)
```

---

interdaycv

*Compute Interday Coefficient of Variation*

---

**Description**

This function computes the interday coefficient of variation

**Usage**

```
interdaycv(df)
```

**Arguments**

**df** Data frame read through readfile

**Value**

A numeric value representing interday cv

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
interdaycv(mydata)
```

---

**interdaysd***Compute Interday Standard Deviation*

---

**Description**

This function computes the interday standard deviation

**Usage**

```
interdaysd(df)
```

**Arguments**

**df** Data frame read through readfile

**Value**

A numeric value representing interday sd

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
interdaysd(mydata)
```

---

---

**intradaycv***Compute Intraday Coefficient of Variation*

---

**Description**

This function computes the intraday coefficient of variation summary statistics: mean, median, standard deviation of all days in data

**Usage**

```
intradaycv(df)
```

**Arguments**

**df** Data frame read through readfile

**Value**

A data frame containing the mean, median, and standard deviation of the intraday coefficients of variation.

## Examples

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
intradaycv(mydata)
```

**intradaysd**

*Compute Intraday Standard Deviation*

## Description

This function computes the intraday standard deviation summary statistics: mean, median, standard deviation of all days in data

## Usage

```
intradaysd(df)
```

## Arguments

df	Data frame read through readfile
----	----------------------------------

## Value

A data frame containing the mean, median, and standard deviation of the intraday standard deviations.

## Examples

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
intradaysd(mydata)
```

**J\_index**

*Compute J-index*

## Description

This function computes J-index, a glycemic variability metrix

## Usage

```
J_index(df)
```

## Arguments

df	Data frame read through readfile
----	----------------------------------

**Value**

A numeric value representing J-index

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
J_index(mydata)
```

---

LBGI

*Compute Low Blood Glucose Index***Description**

This function computes the low blood glucose index

**Usage**

```
LBGI(df)
```

**Arguments**

df	Data frame read through readfile
----	----------------------------------

**Value**

A numeric value representing LBGI

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
LBGI(mydata)
```

---

LBGI\_HBGI

*Compute Low Blood Glucose Index***Description**

This function computes the low blood glucose index

**Usage**

```
LBGI_HBGI(df)
```

**Arguments**

df	Data frame read through readfile
----	----------------------------------

**Value**

A data frame containing both the LBGI and HBGI values

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
LBGI_HBGI(mydata)
```

MGE

*Compute Mean of Glycemic Excursions***Description**

This function computes the mean of glycemic excursions, glycemic excursions indicated by standard deviation, default = 1

**Usage**

```
MGE(df, sd = 1)
```

**Arguments**

df	Data frame read through readfile
sd	Standard deviation indicating glycemic excursion, default = 1

**Value**

A numeric value representing MAGE

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
MGE(mydata)
```

---

MGN

*Compute Mean of Normal Glucose*

---

## Description

This function computes the mean of normal glucose, glycemic excursions indicated by standard deviation, default = 1

## Usage

MGN(df)

## Arguments

df Data frame read through readfile

## Value

A numeric value representing MGN

## Examples

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
MGN(mydata)
```

---

plot\_glucose

*Plot Glucose Data*

---

## Description

This function plots glycemic excursions over the time period in which data was collected.

## Usage

plot\_glucose(df)

## Arguments

df Data frame read through readfile

## Value

None

## Examples

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
plot_glucose(mydata)
```

POR

*Compute Percent of Time Outside Range*

## Description

This function computes the percent of time outside range (range in standard deviations from mean, default = 1).

## Usage

```
POR(df, sd = 1, sr = 5)
```

## Arguments

df	Data frame read through readfile
sd	Standard deviation indicating glycemic excursion, default = 1
sr	Sampling rate inverse in minutes of the CGM (default is Dexcom -> 5 minutes)

## Value

A numeric value representing POR

## Examples

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
POR(mydata, sd = 1, sr = 5)
```

readfile

*Read in Data Frame*

## Description

This function reads in a .csv with variable names Timestamp..YYYY.MM.DDThh.mm.ss and Glucose.Value..mg.dL

## Usage

```
readfile(filename)
```

**Arguments**

filename .csv file of data frame to be read

**Value**

transformed data frame for further analysis

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
readfile(mydatafile)
```

---

summary\_glucose *Compute Glucose Summary Statistics*

---

**Description**

This function computes the mean, median, minimum, maximum, first quartile, and the third quartile of an individual's overall glucose levels

**Usage**

```
summary_glucose(df)
```

**Arguments**

df Data frame read through readfile

**Value**

A data frame containing the mean, median, minimum, maximum, quartile1, and quartile3 of glucose levels

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
summary_glucose(mydata)
```

---

<b>TIR</b>	<i>Compute Time Inside Range</i>
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---

### Description

This function computes the time inside range (range in standard deviations from mean, default = 1).

### Usage

```
TIR(df, sd = 1, sr = 5)
```

### Arguments

df	Data frame read through readfile
sd	Standard deviation indicating glycemic excursions, default = 1
sr	Sampling rate inverse in minutes of the CGM (default is the Dexcom -> 5 minutes)

### Value

A numeric value representing TIR

### Examples

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
TIR(mydata, sd = 1, sr = 5)
```

---

<b>TOR</b>	<i>Compute Time Outside Range</i>
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---

### Description

This function computes the time outside range (range in standard deviations from mean, default = 1).

### Usage

```
TOR(df, sd = 1, sr = 5)
```

### Arguments

df	Data frame read through readfile
sd	Standard deviation indicating glycemic excursions, default = 1
sr	Sampling rate inverse in minutes of the CGM (default is the Dexcom -> 5 minutes)

**Value**

A numeric value representing TOR

**Examples**

```
mydatafile <- system.file("extdata", "my_data_file.csv", package = "cgmquantify")
mydata <- readfile(mydatafile)
TOR(mydata, sd = 1, sr = 5)
```

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